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PCT10

## RAW SEQUENCE LISTING

DATE: 08/06/2002

PATENT APPLICATION: US/10/069,056

TIME: 14:45:00

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\08062002\J069056.raw

3 <110> APPLICANT: Nuesch, Jurg  
4 Rommelaere, Jean  
6 <120> TITLE OF INVENTION: Parvovirus NS 1 Variants  
8 <130> FILE REFERENCE: 4121-136  
10 <140> CURRENT APPLICATION NUMBER: 10/069,056  
11 <141> CURRENT FILING DATE: 2002-02-11  
13 <150> PRIOR APPLICATION NUMBER: PCT/EP00/07835  
14 <151> PRIOR FILING DATE: 2000-08-11  
16 <150> PRIOR APPLICATION NUMBER: EP 99 115 161.4  
17 <151> PRIOR FILING DATE: 1999-08-13  
19 <160> NUMBER OF SEQ ID NOS: 18  
21 <170> SOFTWARE: PatentIn version 3.1  
23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 2019  
25 <212> TYPE: DNA  
26 <213> ORGANISM: Wildtype Parvovirus NS1  
28 <400> SEQUENCE: 1  
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31 agtaaccagg aagtgttctc atttgttttt aaaaatgaaa atgttcaact gaatggaaaa 120  
33 gatatcggat ggaatagtta caaaaaagag ctgcaggagg acgagctgaa atctttacaa 180  
35 cgaggagcgg aaactacttg ggaccaaagc gaggacatgg aatgggaaac cacagtggat 240  
37 gaaatgacca aaaagcaagt attcattttt gattcttttg ttaaaaaatg tttatttgaa 300  
39 gtgcttaaca caaagaatat atttcctggg gatgttaatt ggtttgtgca acatgaatgg 360  
41 ggaaaagacc aaggctggca ctgccatgta ctaattggag gaaaggactt tagtcaagct 420  
43 caagggaaat ggtggagaag gcaactaaat gtttactgga gcagatgggt ggtaacagcc 480  
45 tgtaatgtgc aactaacacc agctgaaaga attaaactaa gagaaatagc agaagacaat 540  
47 gagtgggtta ctctacttac ttataagcat aagcaaacca aaaaagacta taccaagtgt 600  
49 gttctttttg gaaacatgat tgcttactat tttttaacta aaaagaaaat aagcactagt 660  
51 ccaccaagag acggaggcta ttttcttagc agtgactctg gctggaaaac taacttttta 720  
53 aaagaaggcg agcgccatct agtgagcaaa ctatacactg atgacatgcg gccagaaacg 780  
55 gttgaaacca cagtaaccac tgcgcaggaa actaagcgcg gcagaattca aactaaaaaa 840  
57 gaagtttcta ttaaaactac acttaaagag ctggtgcata aaagagtaac ctcaccagag 900  
59 gactggatga tgatgcagcc agacagttac attgaaatga tggctcaacc aggtggagaa 960  
61 aacctgctga aaaatacgtc agagatttgt acactaactc tagccagaac caaaacagca 1020  
63 tttgacttaa ttttagaaaa agctgaaacc agcaaaacta ccaacttttc actgcctgac 1080  
65 acaagaacct gcagaatttt tgcttttcat ggctggaact atgttaaagt ttgccatgct 1140  
67 atttgctgtg ttttaaacag acaaggaggc aaaagaaata ctgttttatt tcatggacca 1200  
69 gccagcacag gcaaatctat tattgcacaa gccatagcac aagcagttgg caatgttggt 1260  
71 tgctataatg cagccaatgt aaactttcca ttaatgact gtaccaacaa gaacttgatt 1320  
73 tgggtagaag aagctggtaa ctttggacag caagtaaacc agtttaaagc catttgctct 1380  
75 ggtcaaaacta ttcgcattga tcaaaaagga aaaggcagca aacagattga accaacaacca 1440  
77 gtcatcatga ccacaaatga gaacattaca gtggtcagaa taggctgcga agaaagacca 1500  
79 gaacacactc aaccaatcag agacagaatg cttaacattc atctaacaca taccttgctt 1560

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81 ggtgactttg gtttggttga caaaaatgaa tggcccatga tttgtgcttg gttggtaaag 1620
83 aatggttacc aatctaccat ggcaagctac tgtgctaaat ggggcaaagt tctgattgg 1680
85 tcagaaaact gggcggagcc aaaggtgccaa actcctataa atttactagg ttcggcacgc 1740
87 tcaccattca cgacaccgaa agtacgcct ctcagccaga actatgcact aactccactt 1800
89 gcatcgatc tcgaggacct ggcttttagag ccttgagaca caccaaatac tcctgttgcg 1860
91 ggcactgcag aaaccagaa cactggggaa gctggttcca aagcctgccaa agatggtcaa 1920
93 ctgagcccaa cttggtcaga gatcgaggag gatttgagag cgtgcttcgg tgcggaaccg 1980
95 ttgaagaaag acttcagcga gccgctgaac ttggactaa 2019
98 <210> SEQ ID NO: 2
99 <211> LENGTH: 672
100 <212> TYPE: PRT
101 <213> ORGANISM: Wildtype Parvovirus NS1
103 <400> SEQUENCE: 2
105 Met Ala Gly Asn Ala Tyr Ser Asp Glu Val Leu Gly Ala Thr Asn Trp
106 1 5 10 15
109 Leu Lys Glu Lys Ser Asn Gln Glu Val Phe Ser Phe Val Phe Lys Asn
110 20 25 30
113 Glu Asn Val Gln Leu Asn Gly Lys Asp Ile Gly Trp Asn Ser Tyr Lys
114 35 40 45
117 Lys Glu Leu Gln Glu Asp Glu Leu Lys Ser Leu Gln Arg Gly Ala Glu
118 50 55 60
121 Thr Thr Trp Asp Gln Ser Glu Asp Met Glu Trp Glu Thr Thr Val Asp
122 65 70 75 80
125 Glu Met Thr Lys Lys Gln Val Phe Ile Phe Asp Ser Leu Val Lys Lys
126 85 90 95
129 Cys Leu Phe Glu Val Leu Asn Thr Lys Asn Ile Phe Pro Gly Asp Val
130 100 105 110
133 Asn Trp Phe Val Gln His Glu Trp Gly Lys Asp Gln Gly Trp His Cys
134 115 120 125
137 His Val Leu Ile Gly Gly Lys Asp Phe Ser Gln Ala Gln Gly Lys Trp
138 130 135 140
141 Trp Arg Arg Gln Leu Asn Val Tyr Trp Ser Arg Trp Leu Val Thr Ala
142 145 150 155 160
145 Cys Asn Val Gln Leu Thr Pro Ala Glu Arg Ile Lys Leu Arg Glu Ile
146 165 170 175
149 Ala Glu Asp Asn Glu Trp Val Thr Leu Leu Thr Tyr Lys His Lys Gln
150 180 185 190
153 Thr Lys Lys Asp Tyr Thr Lys Cys Val Leu Phe Gly Asn Met Ile Ala
154 195 200 205
157 Tyr Tyr Phe Leu Thr Lys Lys Lys Ile Ser Thr Ser Pro Pro Arg Asp
158 210 215 220
161 Gly Gly Tyr Phe Leu Ser Ser Asp Ser Gly Trp Lys Thr Asn Phe Leu
162 225 230 235 240
165 Lys Glu Gly Glu Arg His Leu Val Ser Lys Leu Tyr Thr Asp Asp Met
166 245 250 255
169 Arg Pro Glu Thr Val Glu Thr Thr Val Thr Thr Ala Gln Glu Thr Lys
170 260 265 270
173 Arg Gly Arg Ile Gln Thr Lys Lys Glu Val Ser Ile Lys Thr Thr Leu
174 275 280 285

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177 Lys Glu Leu Val His Lys Arg Val Thr Ser Pro Glu Asp Trp Met Met
178      290      295      300
181 Met Gln Pro Asp Ser Tyr Ile Glu Met Met Ala Gln Pro Gly Gly Glu
182 305      310      315      320
185 Asn Leu Leu Lys Asn Thr Leu Glu Ile Cys Thr Leu Thr Leu Ala Arg
186      325      330      335
189 Thr Lys Thr Ala Phe Asp Leu Ile Leu Glu Lys Ala Glu Thr Ser Lys
190      340      345      350
193 Leu Thr Asn Phe Ser Leu Pro Asp Thr Arg Thr Cys Arg Ile Phe Ala
194      355      360      365
197 Phe His Gly Trp Asn Tyr Val Lys Val Cys His Ala Ile Cys Cys Val
198      370      375      380
201 Leu Asn Arg Gln Gly Gly Lys Arg Asn Thr Val Leu Phe His Gly Pro
202 385      390      395      400
205 Ala Ser Thr Gly Lys Ser Ile Ile Ala Gln Ala Ile Ala Gln Ala Val
206      405      410      415
209 Gly Asn Val Gly Cys Tyr Asn Ala Ala Asn Val Asn Phe Pro Phe Asn
210      420      425      430
213 Asp Cys Thr Asn Lys Asn Leu Ile Trp Val Glu Glu Ala Gly Asn Phe
214      435      440      445
217 Gly Gln Gln Val Asn Gln Phe Lys Ala Ile Cys Ser Gly Gln Thr Ile
218      450      455      460
221 Arg Ile Asp Gln Lys Gly Lys Gly Ser Lys Gln Ile Glu Pro Thr Pro
222 465      470      475      480
225 Val Ile Met Thr Thr Asn Glu Asn Ile Thr Val Val Arg Ile Gly Cys
226      485      490      495
229 Glu Glu Arg Pro Glu His Thr Gln Pro Ile Arg Asp Arg Met Leu Asn
230      500      505      510
233 Ile His Leu Thr His His Leu Pro Gly Asp Phe Gly Leu Val Asp Lys
234      515      520      525
237 Asn Glu Trp Pro Met Ile Cys Ala Trp Leu Val Lys Asn Gly Tyr Gln
238      530      535      540
241 Ser Thr Met Ala Ser Tyr Cys Ala Lys Trp Gly Lys Val Pro Asp Trp
242 545      550      555      560
245 Ser Glu Asn Trp Ala Glu Pro Lys Val Pro Thr Pro Ile Asn Leu Leu
246      565      570      575
249 Gly Ser Ala Arg Ser Pro Phe Thr Thr Pro Lys Ser Thr Pro Leu Ser
250      580      585      590
253 Gln Asn Tyr Ala Leu Thr Pro Leu Ala Ser Asp Leu Glu Asp Leu Ala
254      595      600      605
257 Leu Glu Pro Trp Ser Thr Pro Asn Thr Pro Val Ala Gly Thr Ala Glu
258      610      615      620
261 Thr Gln Asn Thr Gly Glu Ala Gly Ser Lys Ala Cys Gln Asp Gly Gln
262 625      630      635      640
265 Leu Ser Pro Thr Trp Ser Glu Ile Glu Glu Asp Leu Arg Ala Cys Phe
266      645      650      655
269 Gly Ala Glu Pro Leu Lys Lys Asp Phe Ser Glu Pro Leu Asn Leu Asp
270      660      665      670
273 <210> SEQ ID NO: 3

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274 <211> LENGTH: 60
275 <212> TYPE: DNA
276 <213> ORGANISM: Part of Parvovirus NS1 Variant
278 <400> SEQUENCE: 3
279 gaagttgcta ttaaaactac acttaaagag ctggtgcata aaagagtaac ctcaccagag      60
282 <210> SEQ ID NO: 4
283 <211> LENGTH: 2019
284 <212> TYPE: DNA
285 <213> ORGANISM: Parvovirus NS1 Variant
287 <400> SEQUENCE: 4
288 atggctggaa atgcttactc tgatgaagtt ttgggagcaa ccaactggtt aaaggaaaaa      60
290 agtaaccagg aagtgttctc atttgttttt aaaaatgaaa atgttcaact gaatggaaaa      120
292 gatatcggat ggaatagtta caaaaaagag ctgcaggagg acgagctgaa atctttacaa      180
294 cgaggagcgg aaactacttg ggaccaaagc gaggacatgg aatgggaaac cacagtggat      240
296 gaaatgacca aaaagcaagt attcattttt gattcttttg ttaaaaaatg tttatttgaa      300
298 gtgcttaaca caagaatat atttcttggt gatgttaatt ggtttgtgca acatgaatgg      360
300 ggaaaagacc aaggctggca ctgccatgta ctaattggag gaaaggactt tagtcaagct      420
302 caagggaaat ggtggagaag gcaactaaat gtttactgga gcagatggtt ggtaacagcc      480
304 tgtaatgtgc aactaacacc agctgaaaga attaaactaa gagaaatagc agaagacaat      540
306 gagtgggtta ctctacttac ttataagcat aagcaaacca aaaaagacta taccaagtgt      600
308 gttctttttg gaaacatgat tgcttactat tttttaacta aaaagaaaat aagcactagt      660
310 ccaccaagag acggaggcta ttttcttagc agtgactctg gctggaaaac taacttttta      720
312 aaagaaggcg agcgccatct agtgagcaaa ctatacactg atgacatgcg gccagaaacg      780
314 gttgaaacca cagtaaccac tgcgcaggaa actaagcgcg gcagaattca aactaaaaaa      840
316 gaagttgcta ttaaaactac acttaaagag ctggtgcata aaagagtaac ctcaccagag      900
318 gactggatga tgatgcagcc agacagttac attgaaatga tggctcaacc aggtggagaa      960
320 aacctgctga aaaatacgct agagatttgt aactaactc tagccagaac caaaacagca     1020
322 tttgacttaa ttttagaaaa agctgaaacc agcaaaactaa ccaacttttc actgcctgac     1080
324 acaagaacct gcagaatttt tgcttttcat ggctggaact atgttaaagt ttgccatgct     1140
326 atttgctgtg ttttaaacag acaaggaggc aaaagaaata ctgttttatt tcatggacca     1200
328 gccagcacag gcaaatctat tattgcacaa gccatagcac aagcagttgg caatgttggt     1260
330 tgcataatg cagccaatgt aaactttcca tttaatgact gtaccaacaa gaacttgatt     1320
332 tgggtagaag aagctggtaa ctttggacag caagtaaacc agtttaaagc catttgetct     1380
334 ggtcaaaacta ttcgcattga tcaaaaagga aaaggcagca aacagattga accaacacca     1440
336 gtcacatga ccacaaatga gaacattaca tgggtcagaa taggctgcga agaaagacca     1500
338 gaacacactc aaccaatcag agacagaatg cttaacattc atctaacaca taccttgccct     1560
340 ggtgactttg gtttggttga caaaaatgaa tggcccatga tttgtgcttg gtttggtaaag     1620
342 aatggttacc aatctaccat ggcaagctac tgtgctaaat ggggcaaagt tcctgattgg     1680
344 tcagaaaact gggcggagcc aaaggtgcc aactcctataa atttactagg ttcggcacgc     1740
346 tcaccattca cgacaccgaa aagtacgcct ctacagccaga actatgcaact aactccactt     1800
348 gcacgcgcatc tcgaggacct ggcttttagag ccttggagca caccaaatac tcctgttgcg     1860
350 ggactgcag aaaccagaa cactggggaa gctggttcca aagcctgcc aagatggtcaa     1920
352 ctgagcccaa cttggtcaga gatcgaggag gatttgagag cgtgcttcgg tgcggaaccg     1980
354 ttgaagaaag acttcagcga gccgctgaac ttggactaa      2019
357 <210> SEQ ID NO: 5
358 <211> LENGTH: 20
359 <212> TYPE: PRT
360 <213> ORGANISM: Part of Parvovirus NS1 Variant
362 <400> SEQUENCE: 5

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364 Glu Val Ala Ile Lys Thr Thr Leu Lys Glu Leu Val His Lys Arg Val
365 1 5 10 15
368 Thr Ser Pro Glu
369 20
372 <210> SEQ ID NO: 6
373 <211> LENGTH: 672
374 <212> TYPE: PRT
375 <213> ORGANISM: Parvovirus NS1 Variant
377 <400> SEQUENCE: 6
379 Met Ala Gly Asn Ala Tyr Ser Asp Glu Val Leu Gly Ala Thr Asn Trp
380 1 5 10 15
383 Leu Lys Glu Lys Ser Asn Gln Glu Val Phe Ser Phe Val Phe Lys Asn
384 20 25 30
387 Glu Asn Val Gln Leu Asn Gly Lys Asp Ile Gly Trp Asn Ser Tyr Lys
388 35 40 45
391 Lys Glu Leu Gln Glu Asp Glu Lys Ser Leu Gln Arg Gly Ala Glu
392 50 55 60
395 Thr Thr Trp Asp Gln Ser Glu Asp Met Glu Trp Glu Thr Thr Val Asp
396 65 70 75 80
399 Glu Met Thr Lys Lys Gln Val Phe Ile Phe Asp Ser Leu Val Lys Lys
400 85 90 95
403 Cys Leu Phe Glu Val Leu Asn Thr Lys Asn Ile Phe Pro Gly Asp Val
404 100 105 110
407 Asn Trp Phe Val Gln His Glu Trp Gly Lys Asp Gln Gly Trp His Cys
408 115 120 125
411 His Val Leu Ile Gly Gly Lys Asp Phe Ser Gln Ala Gln Gly Lys Trp
412 130 135 140
415 Trp Arg Arg Gln Leu Asn Val Tyr Trp Ser Arg Trp Leu Val Thr Ala
416 145 150 155 160
419 Cys Asn Val Gln Leu Thr Pro Ala Glu Arg Ile Lys Leu Arg Glu Ile
420 165 170 175
423 Ala Glu Asp Asn Glu Trp Val Thr Leu Leu Thr Tyr Lys His Lys Gln
424 180 185 190
427 Thr Lys Lys Asp Tyr Thr Lys Cys Val Leu Phe Gly Asn Met Ile Ala
428 195 200 205
431 Tyr Tyr Phe Leu Thr Lys Lys Lys Ile Ser Thr Ser Pro Pro Arg Asp
432 210 215 220
435 Gly Gly Tyr Phe Leu Ser Ser Asp Ser Gly Trp Lys Thr Asn Phe Leu
436 225 230 235 240
439 Lys Glu Gly Glu Arg His Leu Val Ser Lys Leu Tyr Thr Asp Asp Met
440 245 250 255
443 Arg Pro Glu Thr Val Glu Thr Thr Val Thr Thr Ala Gln Glu Thr Lys
444 260 265 270
447 Arg Gly Arg Ile Gln Thr Lys Lys Glu Val Ala Ile Lys Thr Thr Leu
448 275 280 285
451 Lys Glu Leu Val His Lys Arg Val Thr Ser Pro Glu Asp Trp Met Met
452 290 295 300
455 Met Gln Pro Asp Ser Tyr Ile Glu Met Met Ala Gln Pro Gly Gly Glu
456 305 310 315 320

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VERIFICATION SUMMARY

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